

WHAT IS CLAIMED IS:

1 1. A method of screening drug candidates comprising:
2 a) providing a cell that expresses an expression profile gene selected from
3 the group selected of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1, NAB2,
4 neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83, ApoE,
5 Aeg-2, CD72, cyclin D2, lck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes, c-fos,
6 TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF, TIS7,
7 TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13, kir/gem,
8 EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLF, LKLF, EFP, bcl-3,
9 caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47, NAG,
10 scd2, kappa 0 ig, iap38, G7e, B29, and SCD2;
11 b) adding a drug candidate to the cell; and
12 c) determining the effect of the drug candidate on the expression of the
13 expression profile gene.

1 2. A method according to claim 1 wherein the determining comprises
2 comparing the level of expression in the absence of the drug candidate to the level of
3 expression in the presence of the drug candidate.

1 3. A method according to claim 1 wherein the cell expresses an
2 expression profile gene set of at least one expression profile gene, and the effect of the
3 drug candidate on the expression of the set is determined.

1 4. A method according to claim 3 wherein the set comprises a
2 tolerance set comprising carb anh II, IgD, CD72, SATB1, ApoE, CD83, cyclin D2, Cctq,
3 MEF-2C, TGIF, Aeg-2, Egr-1, lck, Egr-2, E2-20K, pcp-4, kappa V, neurogranin, NAB2,
4 gfi-1 hIP-30, TRAP, bmk, CD36, Evi-2, vimentin, Ly6E.1, and c-fes.

1 5. A method according to claim 4 wherein the expression of hIP-30,
2 TRAP, bmk, CD36, Evi-2, and c-fes are decreased and the expression of carb anh II,
3 CD72, SATB1, ApoE, CD83, cyclin D2, Cctq, MEF-2C, TGIF, Aeg-2, Egr-1, lck, Egr-2,
4 E2-20K, pcp-4, kappa V, neurogranin, NAB2, gfi-1 are increased as a result of the
5 introduction of the drug candidate.

1 6. A method according to claim 3 wherein the set comprises a
2 stimulation set comprising Egr-1, Egr-2, NAB2, mafK, LRG-21, c-fos, c-myc, Stra13,
3 AhR, gadd153, C/EBP beta, TIS11b, TIS11, gfi-1, EZF, Nur77, LSIRF, SNK, PAC-1,
4 kir/gem, MacMARCKS, PEP, MKP1, hRab30, MIP-1b, MIP-1a, EB12, BL34, IL1-R2,
5 TIS7, MyD116, A1, uPAR, RP105, Evi-2 4F2, CD72, Id3, BKLF, LKLF, EFP, Stat1,
6 bcl-3, hRhoH, TRAF5, SLAP, LT-beta, IFNg-RII, GILZ. Caspase 2, gadd45, CDC47,
7 NAG, scd2, kappa 0 ig, B29, iap38, G7e, and hIFI-204.

1 7. A method according to claim 6 wherein the expression of Id3,
2 BKLF, LKLF, EFP, Stat1, bcl-3, hRhoH, TRAF5, SLAP, LT-beta, IFNg-RII, GILZ.
3 Caspase 2, gadd45, CDC47, NAG, scd2, kappa 0 ig, B29, iap38, G7e, and hIFI-204 are
4 decreased and the expression of Egr-1, Egr-2, NAB2, mafK, LRG-21, c-fos, c-myc,
5 Stra13, AhR, gadd153, C/EBP beta, TIS11b, TIS11, gfi-1, EZF, Nur77, LSIRF, SNK,
6 PAC-1, kir/gem, MacMARCKS, PEP, MKP1, hRab30, MIP-1b, MIP-1a, EB12, BL34,
7 IL1-R2, TIS7, MyD116, A1, uPAR, RP105, Evi-2 4F2, CD72 are increased as a result of
8 the introduction of the drug candidate.

1 8. A method according to claim 3 wherein the set comprises an
2 immuno suppression set comprising hIFI-204, hRhoH, caspase 2, B29, SLAP, NAG,
3 iap38, gadd45, BKLF, G7e, Id3, scd2, GILZ, Stat1, kappa 0 ig, LT-beta, LKLF, IFNg-
4 RII, mCDC47, EFP, TRAF5, and bcl-3.

1 9. A method according to claim 8 wherein the expression of hIFI-204,
2 hRhoH, caspase 2, B29, SLAP, NAG, iap38, gadd45, BKLF, G7e, Id3, scd2, GILZ, Stat1,
3 kappa 0 ig, LT-beta, LKLF, IFNg-RII, mCDC47, EFP, TRAF5, and bcl-3 are decreased
4 and the expression of LSIRF, kir/gem, MKP1, hRab30, AhR, c-myc, IL1-R2, TIS11b, Evi-
5 2, A1, EB12, MyD116, MacMARCKS, MIP-1b, MIP-1a, PEP, CD72 are increased as a
6 result of the introduction of the drug candidate.

1 10. A method according to claim 8 wherein the immuno suppressive set
2 further comprises c-fos, gadd153, EZF, C/EBP beta, Stra13, NAB2, mafK, and LRG-21.

1 11. A method according to claim 10 wherein the expression of c-fos,
2 gadd153, EZF, C/EBP beta, Stra13, NAB2, mafK, and LRG-21 are increased as a result
3 of the introduction of the drug candidate.

1 12. A method of screening for a bioactive agent capable of binding to a
2 B lymphocyte modulator protein (BLMP), the method comprising combining the BLMP
3 and a candidate bioactive agent, and determining the binding of the candidate agent to the
4 BLMP.

1 13. A method according to claim 11 wherein the BLMP is selected
2 from the group consisting of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1,
3 NAB2, neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83,
4 ApoE, Aeg-2, CD72, cyclin D2, 1ck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes,
5 c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF,
6 TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13,
7 kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLF, LKLF, EFP,
8 bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47,
9 NAG, scd2, kappa 0 ig, iap38, G7e, B29, and SCD2.

1 14. A method for screening for a bioactive agent capable of modulating
2 the activity of a B lymphocyte modulator protein (BLMP), the method comprising
3 combining the BLMP and a candidate bioactive agent, and determining the effect of the
4 candidate agent on the bioactivity of the BLMP.

1 15. A method according to claim 13 wherein the BLMP is selected
2 from the group consisting of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1,
3 NAB2, neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83,
4 ApoE, Aeg-2, CD72, cyclin D2, 1ck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes,
5 c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF,
6 TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13,
7 kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLF, LKLF, EFP,
8 bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47,
9 NAG, scd2, kappa 0 ig, iap38, G7e, B29, and SCD2.

1 16. A method of evaluating the effect of an immunosuppressive drug
2 comprising:
3 a) administering the drug to a patient;
4 b) removing a cell sample from the patient; and
5 c) determining the expression profile of the cell sample.

1 17. A method according to claim 16 further comprising comparing the
2 expression profile to an expression profile of a healthy individual.

1 18. A method according to claim 16 wherein the expression profile
2 includes at least one gene selected from the group consisting of Egr-1, Egr-2, Nur77, c-
3 myc, MIP-1a, MIP-1b, BL34, gfi-1, NAB2, neurogranin, SLAP, A1, E2-20K, SATB1,
4 Cctq, kappa V, pcp-4, TGIF, CD83, ApoE, Aeg-2, CD72, cyclin D2, lck, MEF-2C, bmk,
5 IgD, Evi-2, vimentin, CD36, c-fes, c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B,
6 gadd153, mafK, Ah-R, C/EBP beta, EZF, TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1,
7 PEP, MacMARCKS, SNK, Stra13, kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR,
8 4F2, hRab30, Id3, BKL, LKLF, EFP, bcl-3, caspase 2, GILZ, hIFI-204, hRhoH,
9 TRAF5, LT-beta, IFNg-RII, gadd45, CDC47, NAG, scd2, kappa 0 ig, iap38, G7e, B29,
10 and SCD2.

1 19. An array of probes, comprising a support bearing a plurality of
2 nucleic acid probes complementary to a plurality of mRNAs fewer than 1000 in number,
3 wherein the plurality of mRNA probes includes an mRNA expressed by a gene selected
4 from the group consisting of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1,
5 NAB2, neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83,
6 ApoE, Aeg-2, CD72, cyclin D2, lck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes,
7 c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF,
8 TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13,
9 kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKL, LKLF, EFP,
10 bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47,
11 NAG, scd2, kappa 0 ig, iap38, G7e, B29, and SCD2.

1 20. The array of claim 19, wherein the probes are cDNA sequences.

1 21. The array of claim 19, comprising a plurality of sets of probes,
2 each set of probes complementary to subsequences from a mRNA.